# Raw Sequence Listing Error Summary

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE  The number/laxt at the end of each line "wrapped" down to the next line. This may occur if your file was retirewed in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".  2		ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 09/449204
The number/lext at the end of each line "varapped" down to the next line. This may occur if your file was retrieved in a word processor after receiling it. Please adjust your right margin to .3, as this will prevent "wrapping".  2	ATTI	N: NEW RULES CASES:	PLEASE DISREGARD ENGLISH "ALPHA" HEADERS. WHICH WERE INSERTED BY PTO SOFTWARE
This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wapping".  2			The number/text at the end of each line "wrapped" down to the pext line
Please adjust your right margin to .3, as this will prevent "wapping".  The amino acid numberilext at the end of each line "wapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wapping".  Incorrect Line Length  The rules require that a line not exceed 72 characters in length. This includes spaces.  The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.  This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.  Sequence(s) contain n's or Xan's which represented more than one residue. As per the rules, each n or Xan can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (il) feature section that some may be missing.  T Patentin ver. 2.0 "bug" A "bug" in Patentin version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) Normally, Patentin would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.  Skipped Sequences (OLD RULES) (2) NNORMATION FOR SEQ ID NOX;  (ii) SEQUENCE CHARACTERISTICS*) (iii) SEQUENCE CHARACTERISTICS*) (iv) SEQUEN			
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Please adjust your right margin to .3, as this will prevent "wrapping".	2	_ Wrapped Aminos	
Incorrect Line Length   The rules require that a line not exceed 72 characters in length. This includes spaces.			
4 Misaligned Amino Acid Numbering  The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.  This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.  Sequence(s)			Please adjust your right margin to .3, as this will prevent "wrapping".
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Use of <213>Organism (NEW RULES)  Use of <220>Feature (NEW RULES)  Use of <220> Feature (NEW RULES)  Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" Please explain source of genetic material in <220> t <223> section.  (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)  Patentln ver. 2.0 "bug"  Please do not use "Copy t Disk" function of Patentin version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).		(NEW RULES)	Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
(NEW RULES)  Use of <220>Feature (NEW RULES)  Sequence(s) are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" Please explain source of genetic material in <220> t <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)  Patentln ver. 2.0 "bug"  Please do not use "Copy t Disk" function of Patentln version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).			In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
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Use of <220>Feature (NEW RULES)  Sequence(s) are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" Please explain source of genetic material in <220> t <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)  Patentin ver. 2.0 "bug"  Please do not use "Copy t Disk" function of Patentin version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).		•	Sequence(s) are missing this mandatory field or its response.
Please explain source of genetic material in <220> t <223> section.  (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)  Patentin ver. 2.0 "bug" Please do not use "Copy t Disk" function of Patentin version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).	1	(MENTALES)	1 22
Please explain source of genetic material in <220> t <223> section.  (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)  Patentin ver. 2.0 "bug" Please do not use "Copy t Disk" function of Patentin version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).	12 (	Use of <220>Eastura	Secure 201 - 2 L
Please explain source of genetic material in <220> t <223> section.  (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)  Patentin ver. 2.0 "bug" Please do not use "Copy t Disk" function of Patentin version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).	·- <u></u>	(NFW RIII EQ)	Lies of 2000 to 2003 in MANIDATORY (1940) OR CANIDATORY (1940) OR CANIDATORY
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file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).	13	Patentin ver. 2.0 "bug"	Please do not use "Copy t Disk" function of Patentin version 2.0. This courses a computed
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# RAW SEQUENCE LISTING PATENT APPLICATION US/09/449,204

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